E1 cont'd

HARBERD et al -- Serial No.: 09/485,529

Please replace the paragraph beginning at page 19, line 6, with the following rewritten paragraph:

E2

As is well-understood, homology at the amino acid level is generally in terms of amino acid similarity or identity. Similarity allows for "conservative variation", i.e. substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Similarity may be as defined and determined by the TBLASTN program, of Altschul et al. (1990) J. Mol. Biol. 215: 403-10, which is in standard use in the art, or more preferably GAP (Program Manual for the Wisconsin Package, Version 8, September 1994, Genetics Computer Group, 575 Science Drive, Madison, USA), which uses the algorithm of Needleman and Wunsch to align sequences. Suitable parameters for GAP include the default parameters, a gap creation penalty = 12 and gap extension penalty = 4, or gap creation penalty 3.00 and gap extension penalty 0.1. Homology may be over the full-length of the Rht sequence of Figure 3b, or may more preferably be over a contiguous sequence of 10 amino acids compared with DVAQKLEQLE (SEQ ID NO:4), and/or a contiguous sequence of

17 amino acids, compared with the 17 amino acids underlined in Figure 3b, and/or a contiguous sequence of 27 amino acids compared with DELLAALGYKVRASDMADVAQKLEQLE (SEQ ID NO:56), or a longer sequence, e.g. about 30, 40, 50 or more amino acids, compared with the amino acid sequence of Figure 3b and preferably including the underlined 17 amino acids and/or DVAQKLEQLE (SEQ ID NO:4).

Please replace the paragraph beginning at page 20, line 6, with the following rewritten paragraph:

At the nucleic acid level, homology may be over the full-length or more preferably by comparison with the 30 nucleotide coding sequence within the sequence of Figure 3a and encoding the sequence DVAQKLEQLE (SEQ ID NO:4) and/or the 51 nucleotide coding sequence within the sequence of Figure 3a and encoding the 17 amino acid sequence underlined in Figure 3b, or a longer sequence, e.g. about, 60, 70, 80, 90, 100, 120, 150 or more nucleotides and preferably including the 51 nucleotide of Figure 3 which encodes the underlined 17 amino acid sequence of Figure 3b.

Please replace the paragraph beginning at page 25, line 8, with the following rewritten paragraph:

If need be, stringency can be increased by increasing the temperature of the washes, and/or reducing or even omitting altogether, the SSC in the wash solution.

E3

Please replace the paragraph beginning at page 25, line 16, with the following rewritten paragraph:

E4

Homologues to rht mutants are also provided by the present invention. These may be mutants where the wild-type includes the 17 amino acids underlined in Figure 3b, or a contiguous sequence of 17 amino acids with at least about 10 (more preferably 11, 12, 13, 14, 15, 16 or 17) which have similarity or identity with the corresponding residue in the 17 amino acid sequence underlined in Figure 3, but the mutant does not. Similarly, such mutants may be where the wild-type includes DVAQKLEQLE or a contiguous sequence of 10 amino acids with at least about 5 (more preferably 6, 7, 8 or 9) which have similarity or identity with the corresponding residue in the sequence DVAQKLEQLE, but the mutant does not. Nucleic acid encoding such mutant polypeptides may on expression in a plant confer a phenotype which is insensitive or unresponsive to treatment of the plant with GA, that is a mutant phenotype which is not overcome or there is no reversion to wild-type phenotype on treatment of the plant with GA (though there

E4 cont'd may be some response in the plant on provision or depletion of GA).

Page 41, before the paragraph beginning at line 23, insert the following new heading:

Brief Description of the Drawings

Please replace the paragraph beginning at page 42, line 1, with the following rewritten paragraph:

E5 Figures 2a-2c. DNA sequences from C15-1, 14a1 and 5a1:

Please replace the paragraph beginning at page 42, line 12, with the following rewritten paragraph:

E6 Figures 3a and 3b. Rht sequences:

Please replace the paragraph beginning at page 42, line 23, with the following rewritten paragraph:

E7 Figures 4a and 4b. D39460 sequence:

Please replace the paragraph beginning at page 43, line 10, with the following rewritten paragraph:

E8 Figures 6a and 6b. Rice EST sequence:

HARBERD et al -- Serial No.: 09/485,529

Please replac the paragraph beginning at page 43, line 18, with the following rewritten paragraph:

E9 Figures 7a and 7b. Wheat C15-1 cDNA:

Please replace the paragraph beginning at page 43, line 26, with the following rewritten paragraph:

E10 Figures 8a and 8b. Wheat 5a1 genomic clone:

Please replace the paragraph beginning at page 44, line 6, with the following rewritten paragraph:

E11 Figures 9a and 9b. Maize 1a1 genomic clone:

Please replace the paragraph beginning at page 44, line 19, with the following rewritten paragraph:

E12 Figures 11a-11d. Sequences of maize D8 alleles:

Please replace the paragraph beginning at page 45, line 4, with the following rewritten paragraph:

E13 Figures 12a and 12b. Wheat rht-10 allele:

Please replace the paragraph beginning at page 47, line 3, with the following rewritten paragraph:

E14 Figure 2a gives the complete (single-pass) DNA sequence of cDNA C15-1. We have also obtained DNA sequence for C15-10;

it is identical with that of C15-1, and is therefore not shown. Figures 2b and 2c show original data from individual sequencing runs from clones 14a1 and 5a1. The sequences shown in Figure 2 can be overlapped to make a composite DNA sequence, shown in Figure 3a. This sequence displays strong homology with that of Arabidopsis GAI, as revealed by a comparison of the amino acid sequence of a predicted translational product of the wheat sequence (Rht) with that of GAI (GAI), shown in Figure 3b. In particular, the predicted amino acid sequence of the presumptive Rht reveals a region of near-identity with GAI over the region that is missing in gai (Figure 4). Figure 4 reveals that the homology that extends beyond the gai deletion region in the rice EST is also conserved in Rht (DVAQKLEQLE (SEQ ID NO:4)), thus indicating that this region, in addition to that found in the gai deletion, is involved in GA signal-transduction. This region is not found in SCR, another protein that is related in sequence to GAI but which is not involved in GA signalling. The primers used in the above sequencing experiments are shown in Table 1.